

Figure 1A
Neutrokine- α

1	AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAAGCCCTGCCATGTAGTGCACGCAGGAC	60
61	ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATCTAAAGGCC	120
121	CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC	180
1	M D D S T E R E Q S R L	12
181	TTACTTCTTGCCCTTAAGAAAAGAGAAGAAATGAACTGAAGGAGTGTGTTTCCATCCTCC	240
13	T S C L K K R E E M K L K E C V S I L P	32
	CD-I	
241	CACGGAAGGAAAGCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT	300
33	R K E S P S V R S S K D G K L L A A T L	52
	CD-I	
301	TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTCTACCAGGTGGCCGCC	360
53	L L A L L S C C L T V V S F Y Q V A A L	72
361	TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC	420
73	Q G D L A S L R A E L Q G H H A E K L P	92
	CD-II	
421	CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC	480
93	A G A G A P K A G L E E A P A V T A G L	112
	CD-III	
	#	
481	TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA	540
113	K I F E P P A P G E G N S S Q N S R N K	132
541	AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG	600
133	R A V Q G P E E T V T Q D C L Q L I A D	152
	CD-IV	
601	ACAGTGAACACCAACTATACAAAAAGGATCTTACACATTGTTCATGGCTTCTCAGCT	660
153	S E T P T I Q K G S Y T F V P W L L S F	172
	CD-V	
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATGGTCAAAGAAACTGGTT	720
173	K R G S A L E E K E N K I L V K E T G Y	192
	CD-V	CD-VI
721	ACTTTTATATATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	F F I Y G Q V L Y T D K T Y A M G H L I	212
	CD-VI	CD-VII
781	FTCAGAGGAAGAAGGTCCATGTCTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT	840
213	Q R K K V H V F G D E L S L V T L F R C	232
	CD-VII	CD-VIII
	#	
841	GTATTCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAA	900
233	I Q N M P E T L P N N S C Y S A G I A K	252
	CD-VIII	CD-IX

Figure 1B
Neutrokin-α

901	AACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAAATGCACAAATATCAC	960
253	<u>L E E G D E L Q L A I P R E N A Q I S L</u>	272
	CD-X	
961	TGGATGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGT	1020
273	<u>D G D V T F F G A L K L L</u>	285
	CD-XI	
1021	CTGTAGCTATTTTCTCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA	1080
1081	CCAAAAAAAAAAAAAAAAAAAAA	1100



	10	20	30	
1	M S T E S M I R D V E L	- - - - -	- - - - - A E E A	TNFAalpha
1	M - - - - -	- - - - -	- - - - - T P P E R L	TNFBbeta
1	M G A - - - - -	- - - - -	- - - - -	LTbeta
1	M Q Q P F N Y P Y P Q I Y W - V D S S A S S P W A P P G T V			FasLigand
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokine alpha
1	M D D S T E R E Q S R L	T S C L K K R E E M K L	K E C V S I	Neutrokine alphaSV
	40	50	60	
17	L P K K T G G P Q - - G S R R - - - - -			TNFAalpha
8	F - - - - -	- - - - -	- - - - -	TNFBbeta
4	- - - - L G L E G R G G - - - - -			LTbeta
30	L P C P T S V P R R P G Q R R P P P P P P P P L P P P P P			FasLigand
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokine alpha
31	L P R K E S P S V R S S K D - - - G K L L A A T L L L A L L			Neutrokine alphaSV
	70	80	90	
30	- - - - -	- - - - - C L F L S L F S		TNFAalpha
9	- - - - - L P R V R G T T L H L L L L G L L L V L L P			TNFBbeta
12	- - - - - - R L Q G R G S L L A V A G A T S L V T			LTbeta
60	P P P L P P L P L P P L K K R G N H S T G L C L L V M F F M			FasLigand
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokine alpha
58	S C C L T V V S F Y Q V A A L Q G D L A S L R A E L Q G H H			Neutrokine alphaSV
	100	110	120	
38	F L - - I V A G A T T L F C L L H F G V I G P Q R E E F P R			TNFAalpha
31	G A Q G L P G V G L - - - - -			TNFBbeta
32	L L L A V P I T V L A V L A L V P Q D Q G G L V T E T A D P			LTbeta
90	V L V A L V G L G L G M F Q L F H L Q K E L A E L R E S T S			FasLigand
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokine alpha
88	A E K L P A G A G A P K A G L E E A P A V T A G L K I F E P			Neutrokine alphaSV
	130	140	150	
66	D L S L I S - P L A - Q A V R S S S R T P S D - - - K P V A			TNFAalpha
41	- - - T P S - A A Q - T A R Q H P K M H L A H S T L K P A A			TNFBbeta
62	G A Q A Q Q - G L G F Q K L P E E E P E T D L S P G L P A A			LTbeta
120	Q M H T A S - S L E - K Q I G H P S P P P E K K E L R K V A			FasLigand
118	P A P G E G N S S Q N S R N K R A V Q G P E E T V T Q D C L			Neutrokine alpha
118	P A P G E G N S S Q N S R N K R A V Q G P E E T - - - - -			Neutrokine alphaSV
	160	170	180	
91	H V V A N P Q A E G - Q - - - - - L Q W L N R R A N A L L			TNFAalpha
66	H L I G D P S K Q N - S - - - - - L L W R A N T D R A F L			TNFBbeta
91	H L I G A P L K - G Q G - - - - - L G W E T T K E Q A F L			LTbeta
148	H L T G K S N S R S M P - - - - - L E W E D T Y G I V L L			FasLigand
148	Q L I A D S E T P T I Q K G S Y T F V P W L - - - - L S F K			Neutrokine alpha
142	- - - - - - - - - - - G S Y T F V P W L - - - - L S F K			Neutrokine alphaSV

	190	200	210	
114	A N G V E L R D N - Q L V V P S E G L Y L I Y S Q V L F K G	TNFalpha		
89	Q D G F S L S N N - S L L V P T S G I Y F V Y S Q V V F S G	TNFbeta		
114	T S G T Q F S D A E G L A L P Q D G L Y Y L Y C L V G Y R G	Lfbeta		
172	- S G V K Y K K G - G L V I N E T G L Y F V Y S K V Y F R G	FasLigand		
174	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D	Neutrokin alpha		
155	R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L Y T D	Neutrokin alphaSV		
	220	230	240	
143	Q G C P - - - - S T H V L L T H T I S R I A V S Y Q T K	TNFalpha		
118	K A Y S P - - K A T S S P L Y L A H E V Q L F S S Q Y P F H	TNFbeta		
144	R A P P G G G D P Q G R S V T L R S S L Y R A G G A Y G P G	Lfbeta		
200	Q S C N - - - - N L P L S H K V Y M R N S K Y P Q D	FasLigand		
204	K T Y A M G - - - - H L I Q R K K V H V F G D E L S - -	Neutrokin alpha		
185	K T Y A M G - - - - H L I Q R K K V H V F G D E L S - -	Neutrokin alphaSV		
	250	260	270	
167	V N - - L L S A I K S P C Q R E T P E - - G A E A K P W Y E	TNFalpha		
146	V P - - L L S S Q K M V Y P - - - - - G L Q E P W L H	TNFbeta		
174	T P E L L L E G A E T V T P V L D P A R R Q G Y G P L W Y T	Lfbeta		
222	L V - - M M E G K M M S Y C - - - - - T T G Q M W A R	FasLigand		
226	L V T L F R C I Q N M P E T L P N - - - - - - - - N	Neutrokin alpha		
207	L V T L F R C I Q N M P E T L P N - - - - - - - - N	Neutrokin alphaSV		
	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E	TNFalpha		
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P	TNFbeta		
204	S V G F G G L V Q L R R G E R V Y V N I S H P D M V D F A R	Lfbeta		
242	S S Y L G A V F N L T S A D H L Y V N V S E L S L V N F E E	FasLigand		
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokin alpha		
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokin alphaSV		
	310			
223	S G Q V Y F G I I A L	TNFalpha		
196	S - T V F F G A F A L	TNFbeta		
234	- G K T F F G A V M V G	Lfbeta		
272	S - Q T F F G L Y K L	FasLigand		
274	G D V T F F G A L K L L	Neutrokin alpha		
255	G D V T F F G A L K L L	Neutrokin alphaSV		

Figure 3
Neutrokin- α

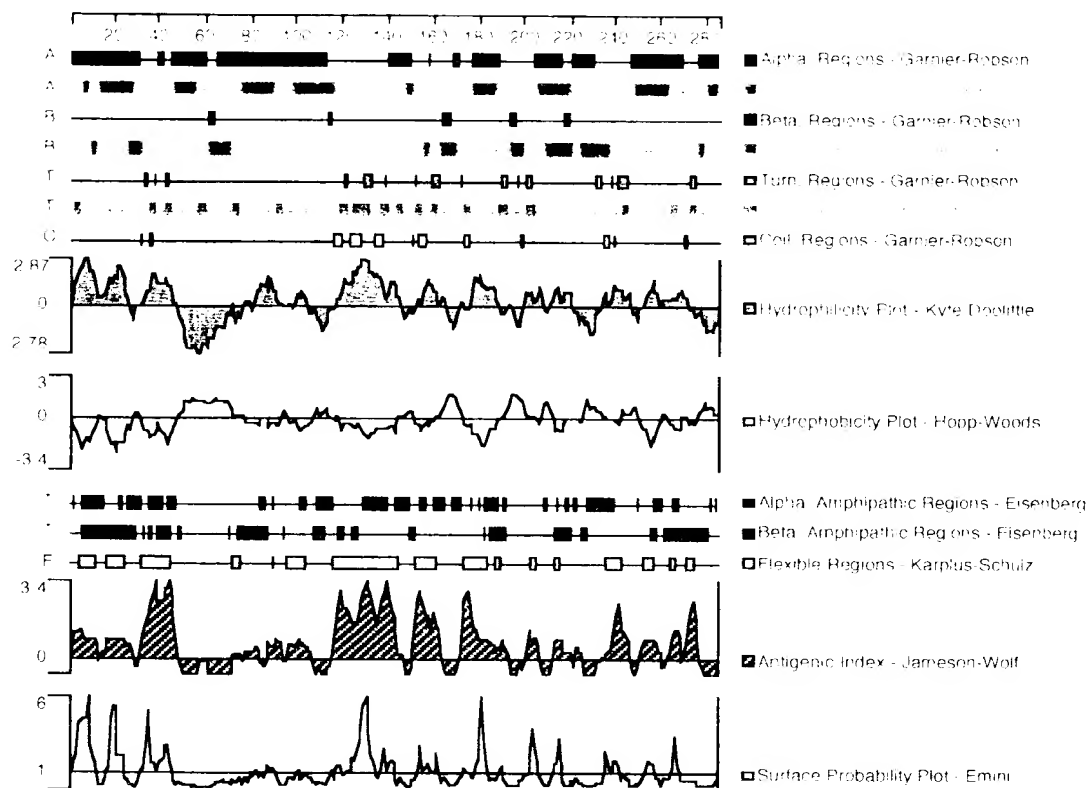


FIGURE 4 A

	1		50
HSOAD55RA	GGNTAACTCT CCTGAGGGGT	GAGCCAAGCC CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT CCTGAGGGGT	GAGCCAAGCC CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG GTTACTTTT	TATATATGGT CAGGTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC GGCCTGGAGG	AAGCTCCAGC TGTCACCGCG
	51		100
HSOAD55R	GTGCACGCAG	GACATCANCA A..ACACANN	NNNCAGGAAA TAATCCATTC
HNEDU15X	GTGCACGCAG	GACATCAACA A..ACACAGA	TAACAGGAAA TGATCCATTC
HSLAH84R	ATACTGATAA	GACCTACGCC ATGGGACATC	TAGTTCAGAG GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC ACCAGCTCCA	GGAGAAGGCA ACTCCAGTCA
	101		150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC	CTTCAAAGTT CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA AGGCCCAAC	CTTCAAAGTT CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT GAGTCTGGTG	ACTTTGTTTC GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG CCGTTCAGGG	TCCAGAAGAA ACAGTCACTC
	151		200
HSOAD55R	TATGGATGAC	TCCACAGAAA GGGAGCAGTC	ACGCCTTACT TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA GGGAGCAGTC	ACGCCTTACT TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC CCAATAATTC	CTGCTATTCA GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNNT GCAGACAGTG	AAACACCAAC TATACAAAAA
	201		250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA CTGNAAGGAG	TGTGTTTCCA TCCTCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA CT.GAAGGAG	TGTGTTTCCA TCCTCCACG
HSLAH84R	CAAACTGGN	AGGAAGGA.. ...GATGAAC	TCCAACCTGC AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA TTTGGGCCAA	GGAATGGAGA GATTTCTTCG
	251		300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC GATCCTCCAA	AGACGGAAAG CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC GATCCTCCAA	AGACGGAAAG CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT GGGATGGAGA	TGTTACATT TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA CTCTTCAGAT	ACTCTTNCT CTCTGGGAAT
	301		350
HSOAD55R	CAACCTTGNT	GNTGGCATTG TGTTCTTGCT	GNCTCAAGGT GGTGTTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG CTGTCTTGCT	GCCTCACGGT GGTGTCTTTC
HSLAH84R	CATTGAACT	GCTGTGACCT NCTTACANCA	NGTGCTGTTN GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA GATTNACACA	TTTGTTCCCA TGGGTNTCTT
	351		400
HSOAD55R
HNEDU15X	TACCAGGTGG	CCGCCCTGCA AGGGGACCTG	GCCAGCCTCC GGGCAGAGCT
HSLAH84R	CTNCCTNTTC	TNTGGTAACC TCTTAGGAAG	GAAGGATTCT TAACTGGGAA
HLTBM08R	AAGTTTTTAA	AGGGGAGTGC CTTAGGAGG	AAAAGGGGAT AAATATTGGC

FIGURE 4B

	401				450
HSOAD55R
HNEDU15X	GCAGGCGCCAC	CACGCGGAGA	AGCTGCCAGC	AGGAGCAGGA	GCCCCCAAGG
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN	GNNANANGNG	GGGNNGTNN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC	AGGTTTNTAT	ANCTGGTAGG
	451				500
HSOAD55R
HNEDU15X	CCGGCCCTGGA	GGAAGCTCCA	GCTGTCACCG	CGGGACTGAA	AATCTTTGAA
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN	GGGNNNGTA	AAAATGGGGC
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG	NCNNTCTTTT	GGGNTGA...
	501				550
HSOAD55R
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT	CAGAACAGCA	GAAATAAGCG
HSLAH84R	CNANGGGGGN	TTTTT.....
HLTBM08R
	551				600
HSOAD55R
HNEDU15X	TGCCGTTTTCAG	GGTCCAGAAG	AAACAGTCAC	TCAAGACTGC	TTGCAACTGA
HSLAH84R
HLTBM08R
	601				650
HSOAD55R
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA	AAGGATCTTA	CACATTTGTT
HSLAH84R
HLTBM08R
	651				700
HSOAD55R
HNEDU15X	CCATGGGCTTC	TCAGCTTTAA	AAGGGGAAGT	GCCCTAGAAG	AAAAAGAGAA
HSLAH84R
HLTBM08R
	701				750
HSOAD55R
HNEDU15X	TAAAAATATTG	GTCAAAGAAA	CTGGTTACTT	TTTTATATAT	GGTCAGGTTT
HSLAH84R
HLTBM08R
	751				800
HSOAD55R
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC	ATCTAATTCA	GAGGAAGAAG
HSLAH84R
HLTBM08R

FIGURE 4C

	801		850
HSOAD55R
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R
HLTBM08R
	851		900
HSOAD55R
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R
HLTBM08R
	901		950
HSOAD55R
HNEDU15X	TTGCAAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R
HLTBM08R
	951		1000
HSOAD55R
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R
HLTBM08R
	1001		1050
HSOAD55R
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R
HLTBM08R
	1051		1100
HSOAD55R
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R
HLTBM08R
	1101		
HSOAD55R		
HNEDU15X	AAAAAA		
HSLAH84R		
HLTBM08R		

Figure 5A
Neutrokinine- α SV

1	ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCCTTACCTTCTGCGCTTAAGAAAAGAGAA	60
1	M D D S T E R E Q S R L T S C L K K R E	20
61	GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCACGGAAGGAAAGCCCTCTGTCCGA	120
21	E M K L K E C V S I L P R K E S P S V R	40
	CD-I	
121	TCCTCCAAAGACGGAAGGTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGTCTG	180
41	S S K D G K L L A A T L L L A L L S C C	60
	CD-I	
181	CTCAGGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACGTGGCCAGCCTCCGG	240
61	L T V V S F Y Q V A A L Q G D L A S L R	80
	CD-II	
241	GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC	300
81	A E L Q G H H A E K L P A G A G A P K A	100
	CD-II	CD-III
301	GGCCTGGAGGAAGCTCCAGCTGTACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA	360
101	G L E E A P A V T A G L K I F E P P A P	120
	CD-III	
	#	
361	GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCCAGGGTCCAGAAGAA	420
121	G E G N S S Q N S R N K R A V Q G P E E	140
421	ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA	480
141	T G S Y T F V P W L L S F K R G S A L E	160
	CD-IV	
481	GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTATATATGGTCAGGTT	540
161	E K E N K I L V K E T G Y F F I Y G Q V	180
	CD-IV	CD-V
541	TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC	600
181	L Y T D K T Y A M G H L I Q R K K V H V	200
	CD-VI	CD-VII
601	TTTGGGGATGAATTGAGTCTGGTGACTTTGTTCGATGTATTCAAAATATGCCTGAAACA	660
201	E G D E L S L V T L F R C I Q N M P E T	220
	CD-VIII	CD-VIII
	#	
661	CTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC	720
221	L P N N S C Y S A G I A K L E E G D E L	240
	CD-IX	CD-X
721	CAACTTGCAATACCAAGAGAAAAATGCACAAATATCAGTGGATGGAGATGTCACATTTT	780
241	Q L A I P R E N A Q I S L D G D V T F F	260
	CD-X	CD-XI
781	GGTGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTCTCCCTTTC	840
261	G A L K L L	266
	CD-XI	

Figure 5B
Neutrokinine- α SV

841 TCCTGTAACCTCTAAGAAGAAGAATCTAACTGAAAAATCCAAAAAAAAAAAAAAAAAAAA 900
901 AAA 903

Figure 6
Neutrokin-αSV

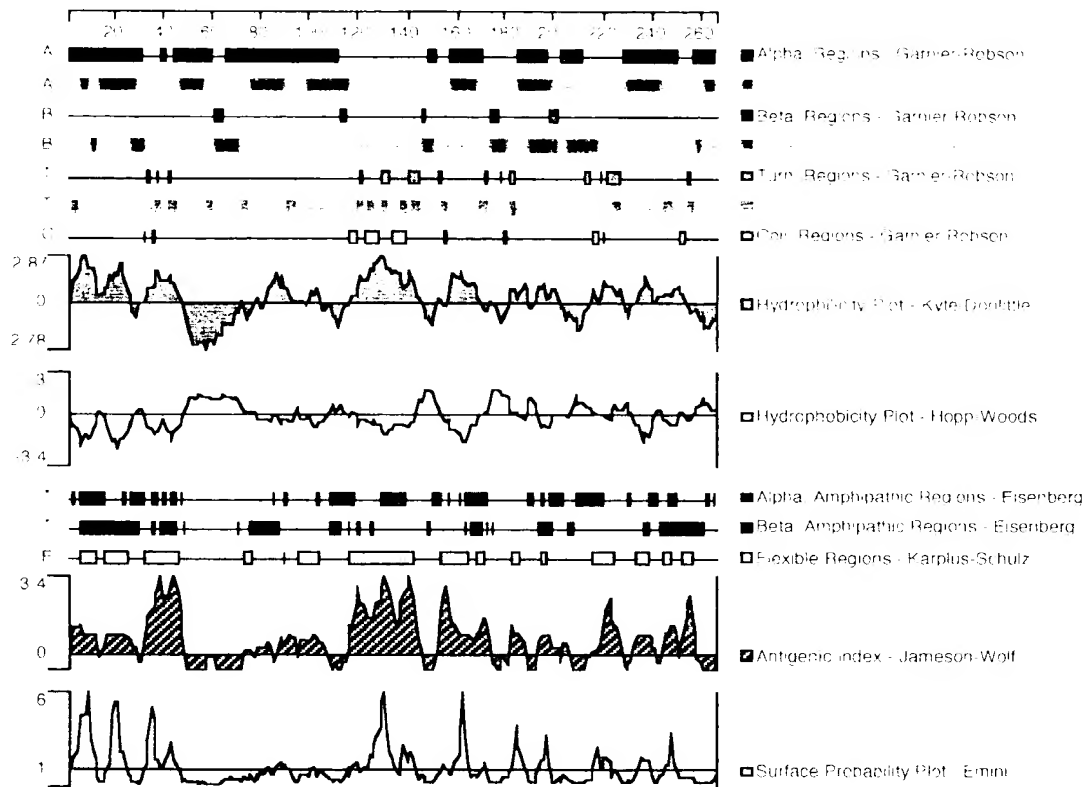


Figure 7

a.

leutokine-
alpha MDDSTEREQSRLTSCLKKREENKLKECVSILPRKESPSVRS 41

Transmembrane Region

SKD GKLLAATLLLLALLSCCLTVVVSFYQVAALQGDLASLRAE 82

LOGHHAEKLPAGAGAPKAGLEEAFAVTA GLKIFEP PAPGEG 123

↓

NSSQNSRNRKRAVQGP EETVT A QDCLQLIADSETPTIQKGSYT 164

April HSV LHLV PINATSK-DDSDVT 134

TNF KPVAHV VANPQAEGQ----- 102

LT α KPA AHLIGDPSKQNS----- 77

A' B' B C

FVPWLLS-----FKRGS ALEEKENKILVKETGYFFIYGQVL 200

EVMWQPA-----LRRGRGLQAQGYGVRIQDAGVYLLYSQVL 170

-LQWLNRRRANALLANGVELRD--NQLVVPSEGLYLIYSQVL 139

-LLWRANTDRAFLQDGFSLSN--NSLLVPTSGIYFVYSQVV 114

D E

YTDKTY-----AMGHLIQRRKKVHVFGDELSLVTLFRCIQNMP 237

FQDVTF-----TMGQVVSRE-----GQGRQETLFRCI RSMP 201

FKGQGCP-----STHVLLTHTISR IAVSYQTKVNLLLSAIKSP 176

FSGKAYS PKATSSPLYLAHEVQLFSSQYPFHVPL LSSQKMV 155

F G

E--TLP-----NNSCYSAGIAKLEE GDELQLAIPRENA 268

SHPDRA-----YNSCYSAGV FHLHQGDILSVIIPRARA 234

CQRETPEGAEAKPWYEPIYLGGVFQLEK GDRLSAEINRPDY 217

YP-----GLQEPWLHSMYHGAA FQLTQGDQLSTHTDGI PH 190

H

QISLDGDVTFFFGALKLL 285

KLNLSPHGTFLGFVKL 250

LDFAESGQVYFGIIAL 233

LVLS- PSTVFFGAFAL 205

b.

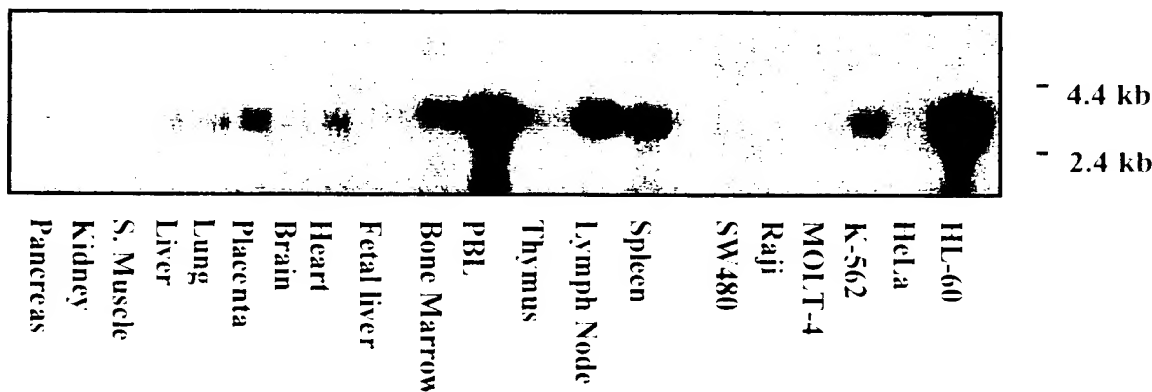
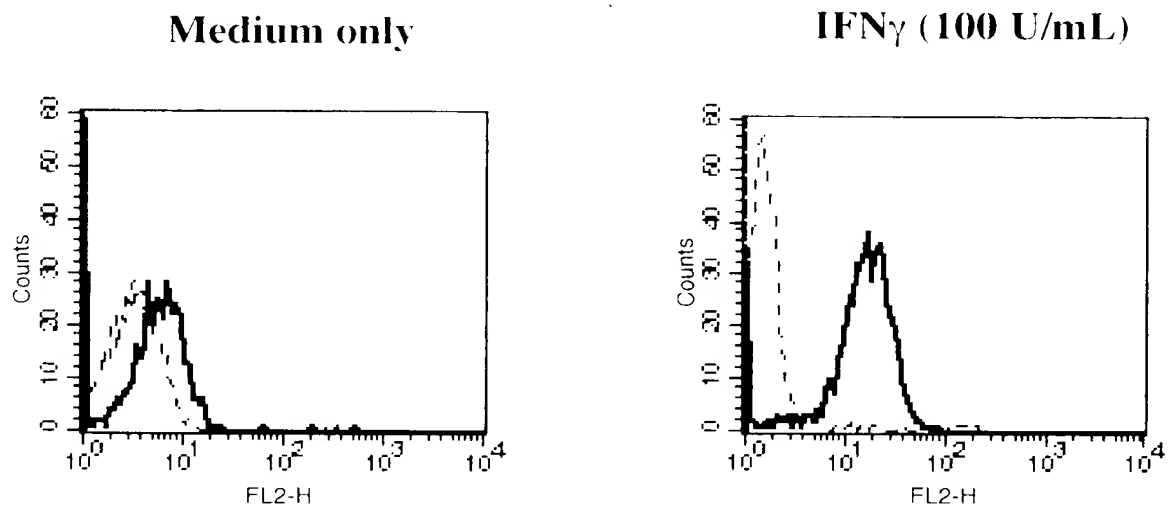


Figure 8

a.



b.

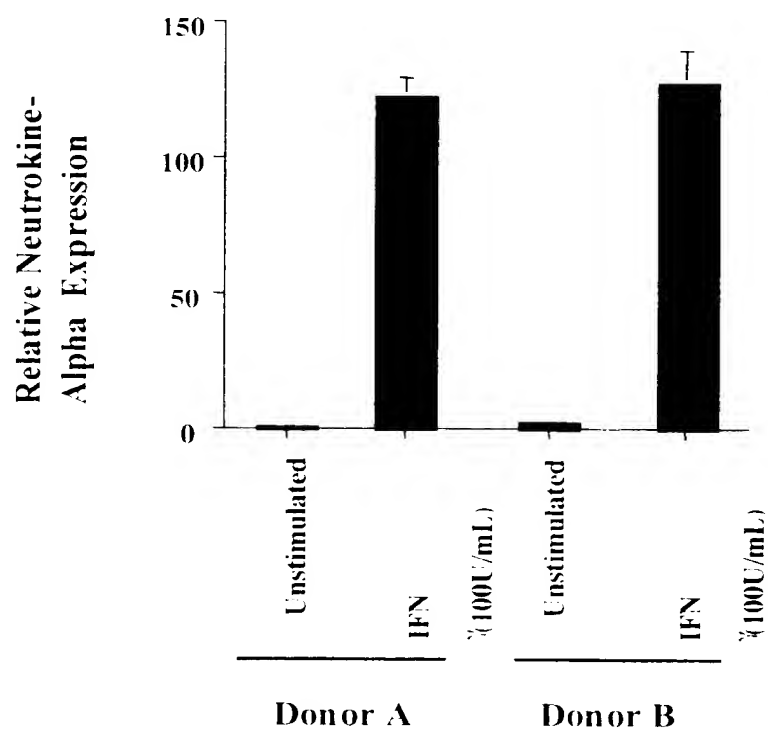
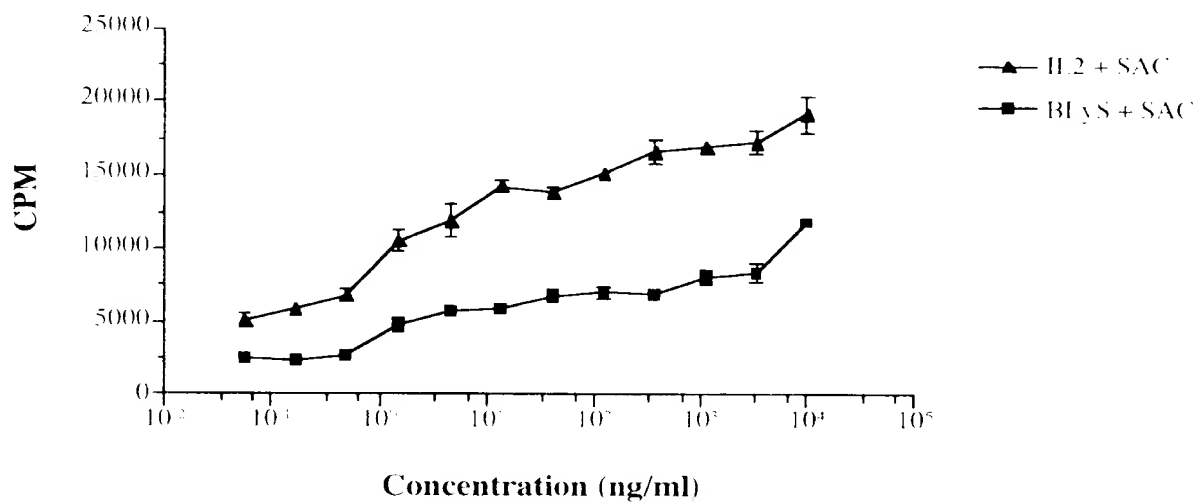


Figure 9

a.



b.

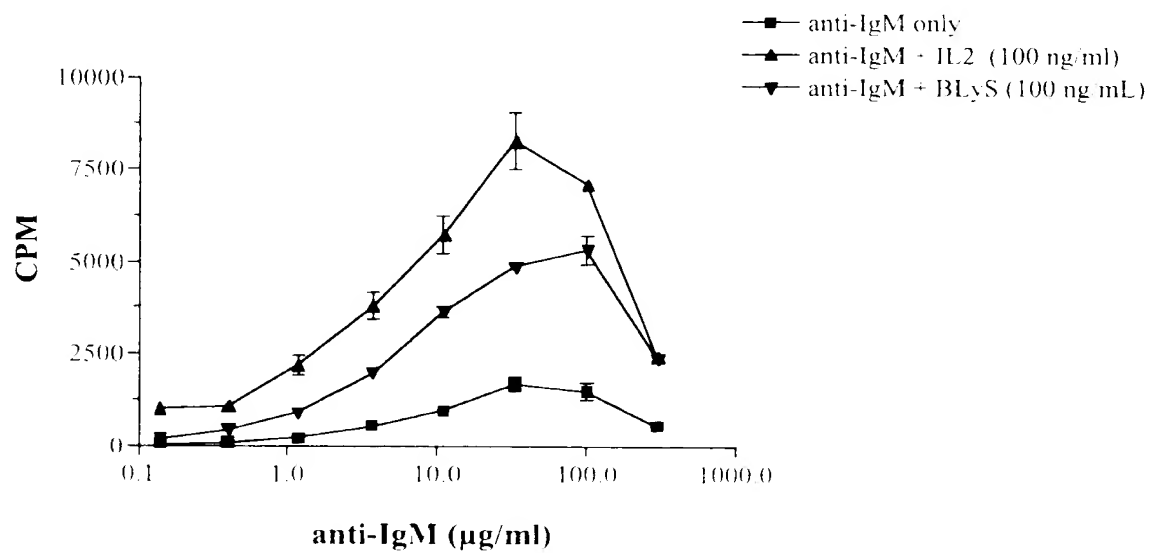
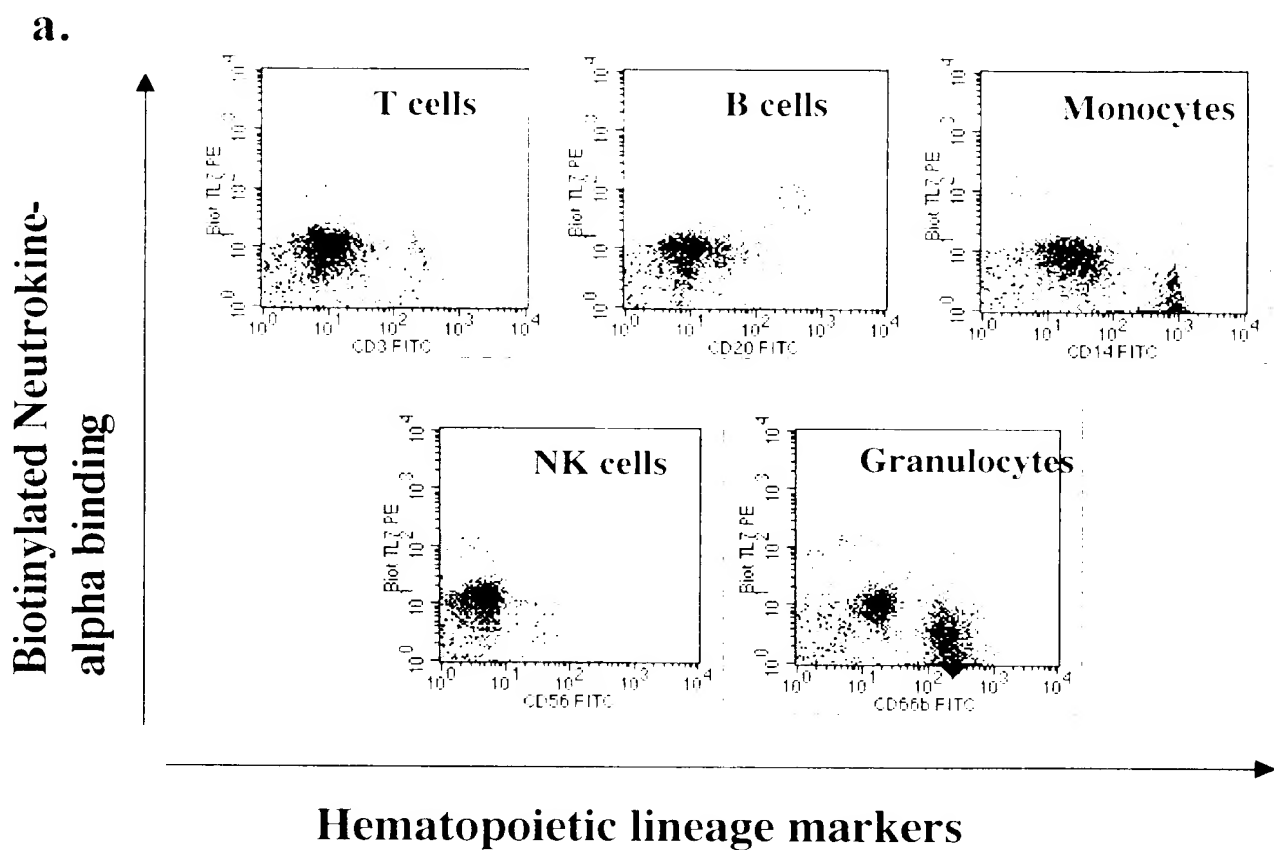


Figure 10



b.

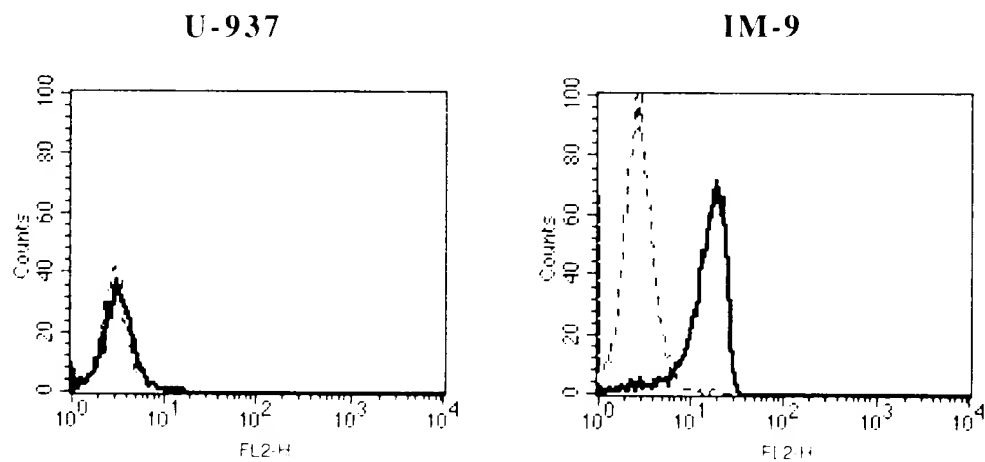


Figure 11

